

**CLAIMS:**

1. An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide  
5 having cysteine proteinase activity, wherein the amino acid sequence of the polypeptide  
and the amino acid sequence of SEQ ID No. 2 have at least 70%, preferably at least 80%,  
sequence identity based on the ClustalW alignment method; or the complement of the  
nucleotide sequence, wherein the complement contains the same number of nucleotides as  
the nucleotide sequence, and the complement and the nucleotide sequence are 100%  
10 complementary.
2. The polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide and  
the amino acid sequence of SEQ ID No. 2 have at least 85%, preferably at least 90%,  
optionally at least 95%, sequence identity based on the ClustalW alignment method.  
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3. The polynucleotide of Claim 1, wherein the nucleotide sequence comprises the nucleotide  
sequence of SEQ ID No. 1.
4. The polynucleotide of Claim 1, wherein the polypeptide comprises the amino acid  
20 sequence of SEQ ID No. 2.
5. An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide  
having cysteine proteinase inhibitor activity, wherein the amino acid sequence of the  
polypeptide and the amino acid sequence selected from the group consisting of SEQ ID  
25 Nos. 4, 10, 12 and 14 have at least 70%, preferably at least 80%, sequence identity based  
on the ClustalW alignment method; or the complement of the nucleotide sequence,  
wherein the complement contains the same number of nucleotides as the nucleotide  
sequence, and the complement and the nucleotide sequence are 100% complementary.
- 30 6. The polynucleotide of Claim 5, wherein the amino acid sequence of the polypeptide and  
the amino acid sequence selected from the group consisting of SEQ ID Nos. 4, 10, 12 and  
14 have at least 85%, preferably at least 90%, optionally at least 95%, sequence identity  
based on the ClustalW alignment method.

7. The polynucleotide of Claim 5, wherein the nucleotide sequence comprises the nucleotide sequence selected from the group consisting of SEQ ID Nos. 3, 9, 11 and 13.
8. The polynucleotide of Claim 5, wherein the polypeptide comprises the amino acid sequence selected from the group consisting of SEQ ID Nos. 4, 10, 12 and 14.
9. An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide having aspartic endoproteinase activity, wherein the amino acid sequence of the polypeptide and the amino acid sequence selected from SEQ ID No. 6 or 8, preferably SEQ ID No. 8, have at least 75%, preferably at least 80%, sequence identity based on the ClustalW alignment method, or the complement of the nucleotide sequence, wherein the complement contains the same number of nucleotides as the nucleotide sequence, and the complement and the nucleotide sequence are 100% complementary.
10. The polynucleotide of Claim 9, wherein the amino acid sequence of the polypeptide and the amino acid sequence selected from SEQ ID No. 6 or 8, preferably SEQ ID No. 8, have at least 85%, preferably at least 90%, optionally at least 95%, sequence identity based on the ClustalW alignment method.
11. The polynucleotide of Claim 9, wherein the nucleotide sequence comprises the nucleotide sequence of SEQ ID No. 5 or 7, preferably SEQ ID No. 7.
12. The polynucleotide of Claim 9, wherein the polypeptide comprises the amino acid sequence of SEQ ID No. 6 or 8, preferably SEQ ID No. 8.
13. An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide having cysteine proteinase activity, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID No. 16 have at least 70%, preferably at least 80%, sequence identity based on the ClustalW alignment method; or the complement of the nucleotide sequence, wherein the complement contains the same number of nucleotides as the nucleotide sequence, and the complement and the nucleotide sequence are 100% complementary.

14. The polynucleotide of Claim 13, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID No. 16 have at least 85%, preferably at least 90%, optionally at least 95%, sequence identity based on the ClustalW alignment method.
- 5 15. The polynucleotide of Claim 13, wherein the nucleotide sequence comprises the nucleotide sequence of SEQ ID No. 15.
16. The polynucleotide of Claim 13, wherein the polypeptide comprises the amino acid sequence of SEQ ID No. 16.
- 10 17. A vector comprising the polynucleotide of any one of Claims 1 to 16.
18. A non-native recombinant DNA construct comprising the polynucleotide of any one of Claims 1 to 16 operably linked to a regulatory sequence.
- 15 19. A method for transforming a cell comprising transforming a cell with the polynucleotide of any one of Claims 1 to 16.
20. A cell comprising the non-native recombinant DNA construct of Claim 18.
- 20 21. The cell of Claim 20, which is a prokaryotic cell, an eukaryotic cell or a plant cell, preferably a coffee cell.
22. A transgenic plant comprising the cell of Claim 20 or 21.
- 25 23. A method for modulating coffee flavour precursor levels in green coffee grains, the method comprising introducing into the coffee plant the non-native recombinant DNA construct of Claim 18.